

Alignment Report of hb71ineup, using Clustal method with PAM250 residue weight table.

**FIG. 1A-1.**

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hB7-1	RIYQKEKKMVL TMMSCMN-----IWPEYKNTIF---DII--NNLSIVLALRPSDEETIEGVVLKYE	122
hB7-2	VVFQDDQENLVNEVYLGKEK--FDSVHSKVMRISF---D-S-DSWTIRLNLOIKKGLVQIIHHKK	110
hB7P-1	YVYVQTSESKTIVV-TYHIPQNSSLENVDSRYRNALMSPAQMRLRDESLRNFNVPQDEQKFHQLV-LSQ	118
hB7P-2	NIIQLTDTKQLVHSFQEQDQG-----SAMANRIALFPDQLAQENASRLQRVRVADEESFTGFV-SIR	127
hB7-H1	AIIVYWEMEDKNI IQFVHGEEDL-KVQHSSYRQPARLKQQLSLNAAQITDVKLQDAQVVRGMI-SYGE	119
hB7-H2 long	AITA-----SLOKV-ENDTSPHREERATLLEEQPLCKASFHPQVQVRDEGQYQII-IYGE	107
hB7-H2 short	AITA-----SLOKV-ENDTSPHREERATLLEEQPLCKASFHPQVQVRDEGQYQII-IYGE	107
hB1N prot	ELRMFRKKVSPAVLHRRQRQDA-AEQMPEYRGRATLVQGGAKLRVALRIRGARVSDDEMTICF--RED	129
hB1N2A1 prot	ELVPMFRSQFSPAFVYKGGRRERT-EEQMEEYRGRITFVSKDISRESVALVIHNIITAQENETMPRCY--	130
hB1N2A2 prot	ELVPMFRSQFSPAFVYKGGRRERT-EEQMEEYRGRITFVSKDINRESVALVIHNIITAQENETMPRCY--	134
hB1N3A2 prot	ELKAVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB1N2.1 prot	ELVPMFRSQFSPAFVYKGGRRERT-EEQMEEYRGRITFVSKDISRESVALVIHNIITAQENETMPRCY--	130
hB1N2.2 prot	ELKAVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB1N2.3 prot	ELRWVSSSLRQVNVVYADGKEVE--YRQSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB1N3A3 prot (hB73)	ELRWVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB1N3A1 prot	ELRWVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB1F5 prot	ELKAVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	131
hB7.3	ELKAVSSSLRQVNVVYADGKEVE--BROSAPYRGRSILRDGITAGKAAALRIHNVITASDSGKYLECYE	129

FIG. 1A-2.

**FIG. 1A-3.**

Alignment Report of hB7 lineage, using Clustal method with PAM250 residue weight table.

hB7-1	INTTWSQD	PETEL	YAVSSKLD	DF	---	NMTTNHSFMCLIKY	221
hB7-2	IMQK-SQ	DNVTE	YDVSISL	SVS	---	PDVTSNMTIFCILETD	217
hB7-1	LQNDTFL	NMRGL	YDWSVLR	RIARTPS	VNI	GCIE	235
hB7-2	TTSQMA	---	NEQGL	FDH	SVLRV	VLGANGTYSC	236
hB7-H1	KTTTNSK	REEK	ENMTSTL	RINTT	NI	IFYDT	210
hB7-H2 long	PANTSHS	RTPES	YQVIT	SVLR	LKPP	CRNFS	193
hB7-H2 short	---	---	---	---	---	---	121
hB7IN prot	TSESRNP	D	EEGL	FTVAASV	IRDTSTKN	VSCYIQNL	245
hB7IN2A1 prot	LKEVSM	PD	ADGL	FMVITTA	IRDKSVRN	MS	256
hB7IN2A2 prot	LKEVSI	AD	ADGL	EMVITTA	IRDKYVRN	VSCSVN	261
hB7IN3A2 prot	VEAPVVA	D	GVGL	YEVAASV	IRGSG	CEGVSC	245
hB7IN2.1 prot	LKEVSM	PD	ADGL	FMVITTA	IRDKSVRN	MS	247
hB7IN2.2 prot	VEAPVVA	D	GVGL	YEVAASV	IRGSG	CEGVSC	245
hB7IN2.3 prot	VEGPVNV	---	GVGL	YAVPPP	VIM	ITSSG	248
hB7IN3A3 prot (hB73)	VEAPVVA	D	GVGL	YAVAA	SVIMR	SGSG	245
hB7IN3A1 prot	VEAPVVA	D	GVGL	YAVAA	SVIMR	SGSG	245
hB7IF5 prot	VEAPVVA	D	GVGL	YAVAA	SVIMR	SGSG	245
hB7.3	VEAPVVA	D	GVGL	YAVAA	SVIMR	SGSG	243

FIG. 1B-1.

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hB7-1	HLRV-NQT	-----FNWNTTKQHFPPDNL	PP	245
hB7-2	KTRLSSP	-----FSIELEDPPPPDHI	----	240
hB7RP-1				235
hB7RP-2				236
hB7-H1				240
hB7-H2 long				218
hB7-H2 short				128
hB7IN prot				284
hB7IN2A1 prot				309
hB7IN2A2 prot				310
hB7IN3A2 prot				313
hB7I.1 prot				295
hB7I.2 prot				313
hB7I.3 prot				318
hB7IN3A3 prot (hB7I.3)				313
hB7IN3A1 prot				313
hB7I5 prot				313
hB7I.3				290

hB7-1	WVAVI	MVLGLLTI	ESIF	WRL	YNERP	RRRN	-----EFS
hB7-2	-----	ILMPIA	VCIM	WINKL	KKK	KILSGEKEF	RRRT
hB7RP-1	SPWMVSM	TVI	AVFI	IFMA	VSICCI	KKL	RRK
hB7RP-2	QPN	AL	AGT	PILLLL	AA	-----	-----
hB7-H1	-----	-----	-----	-----	-----	-----	-----
hB7-H2 long	QPV	AL	AGT	PILLLL	AA	-----	-----
hB7-H2 short	RXXXGPG	XGT	AYFXV	AXSWQ	-----	-----	-----
hB7IN prot	QPN	AL	AGT	PISLLL	AA	-----	-----
hB7IN2A1 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7IN2A2 prot	QRN	AL	ART	PVLLLL	GG	-----	-----
hB7IN3A2 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7I.1 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7I.2 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7I.3 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7IN3A3 prot (hB7I.3)	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7IN3A1 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7I5 prot	QRN	AL	AGT	PVLLLL	GG	-----	-----
hB7I.3	QRN	AL	AGT	PVLLLL	GG	-----	-----

FIG. 1B-2.

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hB7-1	-----SVAITLISVNGIFVICCLTYCFAPRCRER-----RRNERL-----	280
hB7-2	-----PMTITAVLP-----TVIICVMVFCILWKWK-----KKRPRNSY-----	274
hB7P-1	-----PMTITAVLP-----TVIICVMVFCILWKWK-----IGERDK-----	241
hB7P-2	-----PMTITAVLP-----TVIICVMVFCILWKWK-----IGERDK-----	236
hB7-H1	-----LVI-----LGAILL--C-----	250
hB7-H2 long	-----PTM-----LLHIFIPSC-----	230
hB7-H2 short	-----PTM-----LLHIFIPSC-----	140
hB1N prot	SK-----ERLLEELKMKKAT-----	299
hB1N2A1 prot	VK-----EKLQEELRRRTF-----	324
hB1N2A2 prot	-----QQLQEELRRRTF-----	323
hB1N3A2 prot	RKKSS-----	318
hB12.1 prot	VK-----EKLQEELRRRTF-----	310
hB13.2 prot	RKKIQYLTRGEES-----	326
hB13.3 prot	WRKIQYMARGEESSTTKKSALMLKWKALFKPGDKMLQMRVSPCKINWMYSKIYCRKGELIKFISGRVK	388
hB1N3A3 prot (hB73)	WRKIQYMARGEKSLAYHE-----WKMALFKPADVIL-----	344
hB1N3A1 prot	WRSIQYASRGERHSAYNE-----WKKALFKPGEEML-----	344
hB1F5 prot	WRSIQYASRGERHSAYNE-----WKKALFKPADVIL-----	344
hB7.3	-----	290

FIG. 1B-3.

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**FIG. 1C-1.**

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hB7-1	-----RRESVR	286
hB7-2	-----ESEQTKKREKIH	296
hB7R2-1	-----	262
hB7R2-2	-----	256
hB7-H1	-----	264
hB7-H2 long	-----LRKG-----	247
hB7-H2 short	-----LRKQL-----	157
hB1N prot	-----LRKQL-----	331
hB1N2A1 prot	-----LHVDVTLDPDTAHPHLFLYEDSKSVRLDSR	356
hB1N2A2 prot	-----LHVDVVLDPDTAHPDLFLSEDRRSVRRCPFR	355
hB1N3A2 prot	-----LHAADVVLDPDTAHPDLFLSEDRRSVRRGPYR	318
hB72.1 prot	-----LHVDVVLDPDTAHPDLFLSEDRRSVRRCPFR	342
hB73.2 prot	-----NKSALMLK-----	338
hB73.3 prot	GGARDTGFWKDLLSMAQALHAVALKSRKNGRPHGHLLKLSAADVILYPDMANAII LLVSEDQRSVQRAEEP	528
hB1N3A3 prot (hB73)	-----ANAII LLVSEDQRSVQRAEEP	368
hB1N3A1 prot	-----	345
hB7F5 prot	-----ANP ILLVSEDQRSVQRAKEP	368
hB7.3	-----	290

FIG. 1C-2.



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hB7-1	-----IPERSD-----	286
hB7-2	-----L-----	302
hB7P-1	-----VAVAIGW-----	293
hB7P-2	-----ALL-VALAF-----	286
hB7-H1	-----RMMDVK-----	271
hB7-H2 long	-----CQKLYSS-----	255
hB7-H2 short	-----CQKLYSS-----	165
hB1N prot	Q---KLPEKTERFDSWPVVLGRETFTSGRHYWEVEVGDRDWAIGVGRNVMKGGF-DPMTPENGFWAVE	397
hB1N2A1 prot	HLGESVDPNPERFDSQPPVVLGRESFASGKHYYEVEVENVIEWTVGVRDSSVERKGE-VLLIPQNGFWTLE	425
hB1N2A2 prot	Q---RVPDNPERFDSQPPVVLGWESFASGKHYYEVEVENVMVWTVGVGRHSVERKGE-VLLIPQNGFWTLE	421
hB1N2A2 prot	HLGESVDPNPERFDSQPPVVLGRESFASGKHYYEVEVENVIEWTVGVRDSSVERKGE-VLLIPQNGFWTLE	318
hB1N2A2 prot	H---DLPDNPERFEWRYVVLGCESFMSERHYWEVEVGDRKEWHIGVGSKNVERK-KVWVKMTPENGYWTMG	411
hB1N2A3 prot (hB73)	R---DLPDNPERFEWRYVVLGCENFTSGRHYWEVEVGDRKEWHIGVGSKNVERK-KGWVKMTPENGYWTMG	342
hB1N2A1 prot	Q---DLPDNPERFNWHYVVLGCESFISGRHYWEVEVGDRKEWHIGVGSKNVERK-GWVKMTPENGFWTMTMG	595
hB1F5 prot	-----	435
hB7.3	-----	345
	-----	434
	-----	290

FIG. 1C-3.

Alignment Report of hB/lineup, using Clustal method with PAM250 residue weight table.

hB7-1	-----PV	289
hB7-2	-----EAQRVFKSKTSSCDKSDTCF	323
hB7R-1	PETEL-----	298
hB7R-2	DQDSE-----	291
hB7-H1	CGIQDTNSKKQSDTHSE	289
hB7-H2 long	---DTTKPVTTKREVNSAI	274
hB7-H2 short	---DTTKPVTTKREVNSA	182
hB1N prot	LYNGG-YWALTPLRTPAGPPRRVGIFLDYESGDISFYNMNDGSDIYTFSNVTFSGPLRPFFCLWSSG	466
hB1N2A1 prot	MHKQ-Q-YAVSSPDRIIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFVSVPR	485
hB1N2A2 prot	MFGNQ-YALSSPERIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFTVPVR	481
hB1N3A2 prot	-----	318
hB12.1 prot	MHKQ-Q-YAVSSPDRIIPKESLCRVGVFLDYEAGDVSYNMRDRSHIYTCPRSAFSGPDTSE	477
hB13.2 prot	-----	343
hB13.3 prot	LTDGNKYALTEPRTNKKPEPPRKVGIVLDYETGHISFYNATDGSHIYTFLHASSEPLYPVFRILTLE	665
hB1N3A3 prot (hB73)	LTDGNKYALTEPRTNKKPEPPRKVGIVLDYETGEISFYNATDGSHIYTFPHASFSEPLYPVFRILTLE	505
hB1N3A1 prot	-----MRH-----FVK	353
hB1F5 prot	LTDGNKYALTEPRTNKKPKPPKKVGIVLDYETGDISFYNAVDSGSHIHTFLDVSFSEALYPVFRILTLE	504
hB7.3	-----	290

FIG. 1D-1.

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**FIG. 1D-2.**

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289  
323  
309  
317  
290  
274  
183  
527  
528  
524  
320  
530  
360  
734  
585  
353  
514  
291

hb7-1  
hb7-2  
hb7RP-1  
hb7RP-2  
hb7-H1  
hb7-H2 long  
hb7-H2 short  
hbIN prot  
hbIN2A1 prot  
hbIN2A2 prot  
hbIN3A2 prot  
hbT2.1 prot  
hbT3.2 prot  
hbT3.3 prot  
hbIN3A3 prot (hbT3)  
hbIN3A1 prot  
hbT5 prot  
hb7.3  
-----LLS  
-----QEIA.  
-----T  
-----I  
-----T.  
LQMRLHLVK.  
LQARTEALY.  
-----M

FIG. 1D-3.



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[illegible]

Decoration #1': Shade (with dots) residues that match hB7-HI orf exactly.

**FIG. 2B.**

hB7-H1 orf vs hB7-H2 long orf

GAP of : hB7-H1 orf from: 1 to: 873 to: hB7-H2 long orf from: 1 to: 822

Percent Similarity: 58.312 Percent Identity: 58.312

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      .       .       .       .
1  ATGAGGATATTGCTGTCTTTATATT...CATGACCTACTGGCATTGCT  47
      | ||| ||      | | || ||      | ||      | ||| |
1  ...ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCA  47
      .       .       .       .
48  GAACGC.....ATTTACTGTCACGGTTCCCAAGGACCTATATGTGGTAG  91
      || ||      ||| || || || || || || || || || || ||
48  GATAGCAGCTTTATTCACAGTGACAGTCCCTAAGGAAGTGTACATAATAG  97
      .       .       .       .
92  AGTATGGTAGCAATATGACAATTGAATGCAAATCCCAGTAGAAAAACAA 141
      || |||| |||| |||| | |||| || ||      | || ||
98  AGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCAT 147
      .       .       .       .
142 TTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACAT 191
      | |||| | ||| ||| | | || | ||| || |      ||| ||
148 GTGAACCTTGAGCAATAACAGCCAGTTTGCAAAAGGTG....GAAAAT 192
      .       .       .       .
192 TATTCAATTGTGTCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCT 241
      || ||      || ||      || ||
193 GATACA.....TCCCA.....C 205
      .       .       .       .
242 ACAGACAGAGGGCCCGGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCT 291
      || | | || ||| || || || || || || || || || || ||
206 ACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTAGGGAAGGCC 255
      .       .       .       .
292 GCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTG 341
      | | || || | | || || || || || || || || || || ||
256 TCGTTCCACATAGCTCAAGTCCAAGTGAGGGACGAAGGACAGTACCAATG 305
      .       .       .       .
342 CATGATCAGCTATGGTGGTGCC...GACTACAAGCGAATTACTGTGAAAG 388
      ||| |||| |||| || ||| |||| || ||| |||| ||
306 CATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAG 355
      .       .       .       .

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FIG. 3A.

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389 TCAATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGATCCA 438  
| | | | | | | | | | | | | | | | | | | | | |  
356 TCAAAGCTTCCTACAGGAAAATAAAC. . . ACTCACATCCTAAAGGTTCCA 402  
| | | | | | | | | | | | | | | | | | | | | |  
439 GTCACCTCTGAACATGAACTGACATGTCAGGCTGAGGGCTACCCCAAGGC 488  
| | | | | | | | | | | | | | | | | | | | | |  
403 GAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTGGC 452  
| | | | | | | | | | | | | | | | | | | | | |  
489 CGAAGTCATCTGGACAAGCAGTGACCATCAAGTCCTGAGTGGTAAGACCA 538  
| | | | | | | | | | | | | | | | | | | | | |  
453 AGAAGTATCCTGGCCAAAC. GTCAGCGT. . . TCCTG. . . . . CCA 487  
| | | | | | | | | | | | | | | | | | | | | |  
539 CCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGTGACCAGCAC 588  
| | | | | | | | | | | | | | | | | | | | | |  
488 ACACCAGCCACTCCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTT 537  
| | | | | | | | | | | | | | | | | | | | | |  
589 CTGAGAATCAACACAACAACTAATGAGATTTTCTACTGCATTTTAGGAG 638  
| | | | | | | | | | | | | | | | | | | | | |  
538 CTGCGCCTAAAGCCACCCCTGGCAGAACTTCAGCTGTGTGTTCTGGA. 586  
| | | | | | | | | | | | | | | | | | | | | |  
639 ATTAGATCCTGAGGAAAACCATACAGCTGAATTGGTCATCCCAGAACTAC 688  
| | | | | | | | | | | | | | | | | | | | | |  
587 ATACTCACGTGAGGGAA. . CTTAC. . . . . TTTGGCCAGCATTGACCT. T 627  
| | | | | | | | | | | | | | | | | | | | | |  
689 CTCTGGCACATCCTCCAAATGAAAGGACTCACTTGG. TAATTCTGGGAGC 737  
| | | | | | | | | | | | | | | | | | | | | |  
628 CAAAGTCAGATGGAACCCAGGACCCATCCAACCTTGGCTGCTTCACATTT 677  
| | | | | | | | | | | | | | | | | | | | | |  
738 CATCTTATTATGCCTTGGTG. TAGCACTGACATTTCATCTTCCGTTTAAGA 786  
| | | | | | | | | | | | | | | | | | | | | |  
678 CATCCCCTCCTGCATCATTGCTTTTCATTTTCAT. . AGCCACAGTGATAGC 725  
| | | | | | | | | | | | | | | | | | | | | |  
787 AAAGGGAGAATGATGGATGTGAAAAAATGTGGCATCCAAGATACAAACTC 836  
| | | | | | | | | | | | | | | | | | | | | |  
726 CCTAAGA. AAACAACCTCTGTCAAAGCTGTATTCTTCAAAGACACA. AC 773  
| | | | | | | | | | | | | | | | | | | | | |  
837 AAAGAAGCAAAGTGATACACATTTGGAGGAGACGTAA. . . . . 873  
| | | | | | | | | | | | | | | | | | | | | |  
774 AAA. AAGACCTGTCA. CCACAACAAAGAGGGAAGTGAACAGTGCTATCTG 821  
:  
:

FIG. 3B.



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hB7-H1 orf vs hB7-H2 short orf

GAP of : hB7-H1 orf from: 1 to: 873 to: hB7-H2 short orf from: 1 to: 552

Percent Similarity: 59.811 Percent Indentity: 59.811

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      .           .           .           .           .
1  ATGAGGATATTTGCTGTCTTTATATT...CATGACCTACTGGCATTGCT  47
      | ||| ||      | | || ||      ||      || | |
1  ...ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCA  47
      .           .           .           .           .
48 GAACGC.....ATTACTGTACGGTTCCCAAGGACCTATATGTGGTAG  91
      || ||      ||| || || || || || || || || || || ||
48 GATAGCAGCTTTATTACAGTGACAGTCCCTAAGGAAGTGTACATAATAG  97
      .           .           .           .           .
92 AGTATGGTAGCAATATGACAATTGAATGCAAATCCCAGTAGAAAAACAA 141
      || |||| |||| || || | |||| || ||      | || ||
98 AGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCAT 147
      .           .           .           .           .
142 TTAGACCTGGCTGCACTAATTGTCTATTGGGAAATGGAGGATAAGAACA 191
      | |||| | ||| || | | | || || || | || ||
148 GTGAACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTG....GAAAT 192
      .           .           .           .           .
192 TATTCAATTTGTGCATGGAGAGGAAGACCTGAAGGTTCAGCATAGTAGCT 241
      || ||      || ||      || ||
193 GATACA.....TCCCA.....C 205
      .           .           .           .           .
242 ACAGACAGAGGGCCCGCTGTTGAAGGACCAGCTCTCCCTGGGAAATGCT 291
      || | | || || || || || || || || || || || || ||
206 ACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGAAGGCC 255
      .           .           .           .           .
292 GCACTTCAGATCACAGATGTGAAATTGCAGGATGCAGGGGTGTACCGCTG 341
      | | || || | | || || || || || || || || || ||
256 TCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACGTACCAATG 305
      .           .           .           .           .
342 CATGATCAGCTATGGTGGTGCC..GACTACAAGCGAATTACTGTGAAAG 388
      ||| |||| |||| | || | |||| || | || ||||
306 CATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTCTGAAAG 355
      .           .           .           .           .

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**FIG. 4A.**

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389 TC. AATGCCCCATACAACAAAATCAACCAAAGAATTTTGGTTGTGGA... 434
    || || | | || || | | || | | | | | |
356 TCAAAGGTCAGATGGAAC. CCAGGACCCATCCAACCTGGCTGCTTCACAT 404
    . TCCAGTCACCTCTGAACATGAACTGACATGT... CAGGCTGAGGGCTAC 480
    | || | | || | | || | | || | || |
405 TTTTCATCCCCTCCTGCATCATTGCTTTTCATTTTCATAGCCACAGTGATAG 454
    . CCCAAGGCCGAAGTCATCTG. GACAAGCAGTGACCATC. AAGTCCTGAGT 528
    ||| | | || ||| | |||| | | ||| | | |
455 CCCTAAG. AAAACAACCTCTGTCAAAGCTGTATTCTTCAAAGACACAAC 503
    GGTAAGACCACCACCACCAATTCCAAGAGAGAGGAGAAGCTTTTCAATGT 578
    |||| | |||| | |||| | | ||| | | |||
504 AAAAAGAC. . CTGTCACCACAACAAGAGGGAAGTGAA. CAGTGCTATCT 550
    GACCAGCACACTGAGAATCAACACAACAATAATGAGATTTTCTACTGCA 628
    ||
551 GA..... 552
  
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**FIG. 4B.**

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hB7-H2 long vs hB7-H1

GAP of: hB7-H2 long aa from: 1 to: 273 to: hB7-H1 aa from: 1 to: 290

Percent Similarity: 46.792 Percent Identity: 37.358

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1 MIFLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV 50
      : : : : : |||||:|:|:|:|:|:|:|:|:|
1 ..MRIFAVFIFMTYWLLNAFTVTPKDLVVEYGSNMTIECKFPVEKQL 48

51 NLGAITASLQKVENDT.....SPHRERATLLEEQLPLGKAS 86
      .| :| : : : : : | :|:| |:|:| | | |
49 DLAALIVYWEMEDKNIIQFVHGEECLKVQHSSYRQRARLLKDQLSLGNAA 98

87 FHIPQVQVRDEGQYQCIIYGVAWDYKYLTLKVKASYRKINTHILKV. PE 135
      | |...| | |.| | | | | | :|.| | | | | | | |
99 LQITDVKLQDAGVYRCMISYGGA. DYKRITVKVNAPYNKINQRILVDPV 147

136 TDEVELTCQATGYPLAEVSWPN....VSPANTSHSRTPEGLYQVTSVL 180
      | | ||||| | | | | | . | | | : | | : | | |
148 TSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVTSTL 197

181 RLKPPPGRNFSCVF.....WNTHVRELTLASIDLQSQMEPRTHPTWLLHI 225
      |: | | | | | | : | : | | | : |
198 RINTTTNEIFYCTFRRLDPEENHTAELVIPELPLAHPNERTHLV. ILGA 246

226 FIPSCIIAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI 273
      : :| | | . | .| .|: | |
247 ILLCLGVALTFIFRLRKGRMMDVKKCGIQDTNSKKQSDTHLEET.... 290
```

FIG. 5.

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hB7-H2 short vs hB7-H1  
 GAP of : hB7-H2 short aa from: 1 to: 183 to: hB7-H1 aa from: 1 to: 290  
 Percent Similarity: 41.243 Percent Identity: 28.249

1	MIFLLLMLSLELQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHV	50
	: . . . :      : : : : : : : :	
1	..MRIFAVFIFMTYWHLNAFTVTPKDLVVEYGSNMTIECKFPVEKQL	48
51	NLGAITASLQKVENDT.....SPHRERATLLEEQLPLGKAS	86
	.   : : : .   : :   :      .	
49	DLAALIVYWEMEDKNIIQFVHGEECLKVQHSSYRQRARLLKQSLGNAA	98
87	FHIPQVQVRDEGQYQCIIYGVAWDYKYLTLKVKGQMEPRTHPTWLLHIF	136
	...     ...          : ...	
99	LQITDVKLQDAGVYRCMISYGGA. DYKRITVKVNA...PYNKINQRILVV	144
137	IPSCIIAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI...	183
	: : : : : : :   :	
145	DPVTSEHELTCQAEGYPKAEVIWTSSDHQVLSGKTTTTNSKREEKLFNVT	194

⋮

**FIG. 6.**

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hB7-H2 long orf vs hB7-H2 short orf

GAP of: hB7-H2 long orf from: 1 to: 822 to: hB7-H2 short orf from: 1 to: 552

Percent Similarity: 100.000 Percent Identity: 100.000

```

      .           .           .           .
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50

      .           .           .           .
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC  100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC  100

      .           .           .           .
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTG  150
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTG  150

      .           .           .           .
151 AACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTGGAAAATGATACATC  200
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AACCTTGGAGCAATAACAGCCAGTTTGCAAAGGTGGAAAATGATACATC  200

      .           .           .           .
201 CCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGA  250
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 CCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCCTAGGGA  250

      .           .           .           .
251 AGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTAC  300
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
251 AGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTAC  300

      .           .           .           .
301 CAATGCATAATCATCTATGGGGTCGCTGGGACTACAAGTACCTGACTCT  350
    | | | | | | | | | | | | | | | | | | | | | | | | | | | |
301 CAATGCATAATCATCTATGGGGTCGCTGGGACTACAAGTACCTGACTCT  350

      .           .           .           .
351 GAAAGTCAAAGCTTCTACAGGAAAATAAACACTCACATCCTAAAGGTTTC  400
    | | | | | | | |
351 GAAAGTCAAAG..... 361

```

FIG. 7A.

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:

601 GAACTTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGAC 650  
|||||  
362 ..... GTCAGATGGAACCCAGGAC 380

651 CCATCCAACCTGGCTGCTTACATTTTCATCCCCTCCTGCATCATTGCTT 700  
|||||  
381 CCATCCAACCTGGCTGCTTACATTTTCATCCCCTCCTGCATCATTGCTT 430

701 TCATTTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAG 750  
|||||  
431 TCATTTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAG 480

751 CTGTATTCTTCAAAGACACAACAAAAGACCTGTCACCACAACAAAGAG 800  
|||||  
481 CTGTATTCTTCAAAGACACAACAAAAGACCTGTCACCACAACAAAGAG 530

801 GGAAGTGAACAGTGCTATCTGA 822  
|||||  
531 GGAAGTGAACAGTGCTATCTGA 552

FIG. 7B.

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hB7-H2 long vs hB7-H2 short

GAP of: hB7-H2 long aa from: 1 to: 273 to: hB7-H2 short aa from: 1 to: 183  
Percent Similarity: 74.444 Percent Identity: 71.667

```

      . . . . .
1  MIFLLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV  50
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1  MIFLLLMLSLELQLHQIAALFTVTPKELYIIHGNSVTLECNFDTGSHV  50
      . . . . .
51 NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100
      . . . . .
101 QCIIIYGVAWDYKYLTLKVKASY. . RKINTHILKV. PETDEVELTCQATG 147
    | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 QCIIIYGVAWDYKYLTLKVKQMEPRTHPTWLLHIFIPSCIIAFIFIATV 150
      . . . . .
148 YPLAEVSWPNVSPANTSHSRTPEGLYQVTSVLRLKPPPGRNFSCVFWNT 197
    | . . . . . | . . . . . : | | :
151 IALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI..... 183

```

⋮

FIG. 8.

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hB7-H1	MRIFAVFII	MTYWHLLNAFTVTVPKDLVVEYGSNMTIECKFPVEKQ	47
hB7-H2 long	M-IF	LLLMSLELQLHQIAALFTVTVPKELYIIIEHGSNVTLECNFDTGSH	49
hB7-H2 short	M-IE	LLLMSLELQLHQIAALFTVTVPKELYIIIEHGSNVTLECNFDTGSH	49
hB7-H1	LD	AALIVYVEME DKNIIQFVHGEE DLKVQHSSYRQRARLKKDQLSLGNA	97
hB7-H2 long	VNLGAI	ITA-----SLQKVENDTSPHREERATLLEEQLPLGKA	85
hB7-H2 short	VNLGAI	ITA-----SLQKVENDTSPHREERATLLEEQLPLGKA	85
hB7-H1	ALQIITDVKLQDAGVYRCMISYGA	DYKRITVKVNAPYKNINQRILVVDP	146
hB7-H2 long	SFHI	PQVQVRDEEGQYQCIIIIYGVAWDYKYLLIKVKA SYRKINTHLLKVP-P	134
hB7-H2 short	SFHI	PQVQVRDEEGQYQCIIIIYGVAWDYKYLLIKVKG-----	121
hB7-H1	VTSEHELICQAE	GYPKAEVIWISSDHQVLSGKITITNSKREEKLEFNVIST	196
hB7-H2 long	ETDEVELTICQATGYP	LAEVSMPN-----VSVPANITSHSRTPEGLYQVTSV	179
hB7-H2 short	ETDEVELTICQATGYP	LAEVSMPN-----VSVPANITSHSRTPEGLYQVTSV	121
hB7-H1	RINITTNEIFYCTERRIDPEENHTAEL	VIPELP AHPNERTHLVITIGA	246
hB7-H2 long	LSLKPPPGRNESCVFW	-----NTHVRELTLASIDLQSQMEPRTHPTWLHL	224
hB7-H2 short	LSLKPPPGRNESCVFW	-----NTHVRELTLASIDLQSQMEPRTHPTWLHL	134
hB7-H1	TLIL	CLCVALTFT-----ERLRKQ-----RMMDVKKCGIQDTNSKKQSDTHLEE	289
hB7-H2 long	IFIPSC	CI-IAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSAI	273
hB7-H2 short	IFIPSC	CI-IAFIFIATVIALRKQLCQKLYSSKDTTKRPVTTTKREVNSA-	182
hB7-H1	I		290
hB7-H2 long	I		274
hB7-H2 short	I		183

Decoration 'Decoration #1: Shade (with dots) residues that match hB7-H1 exactly.

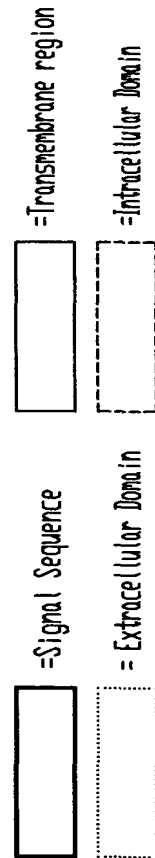
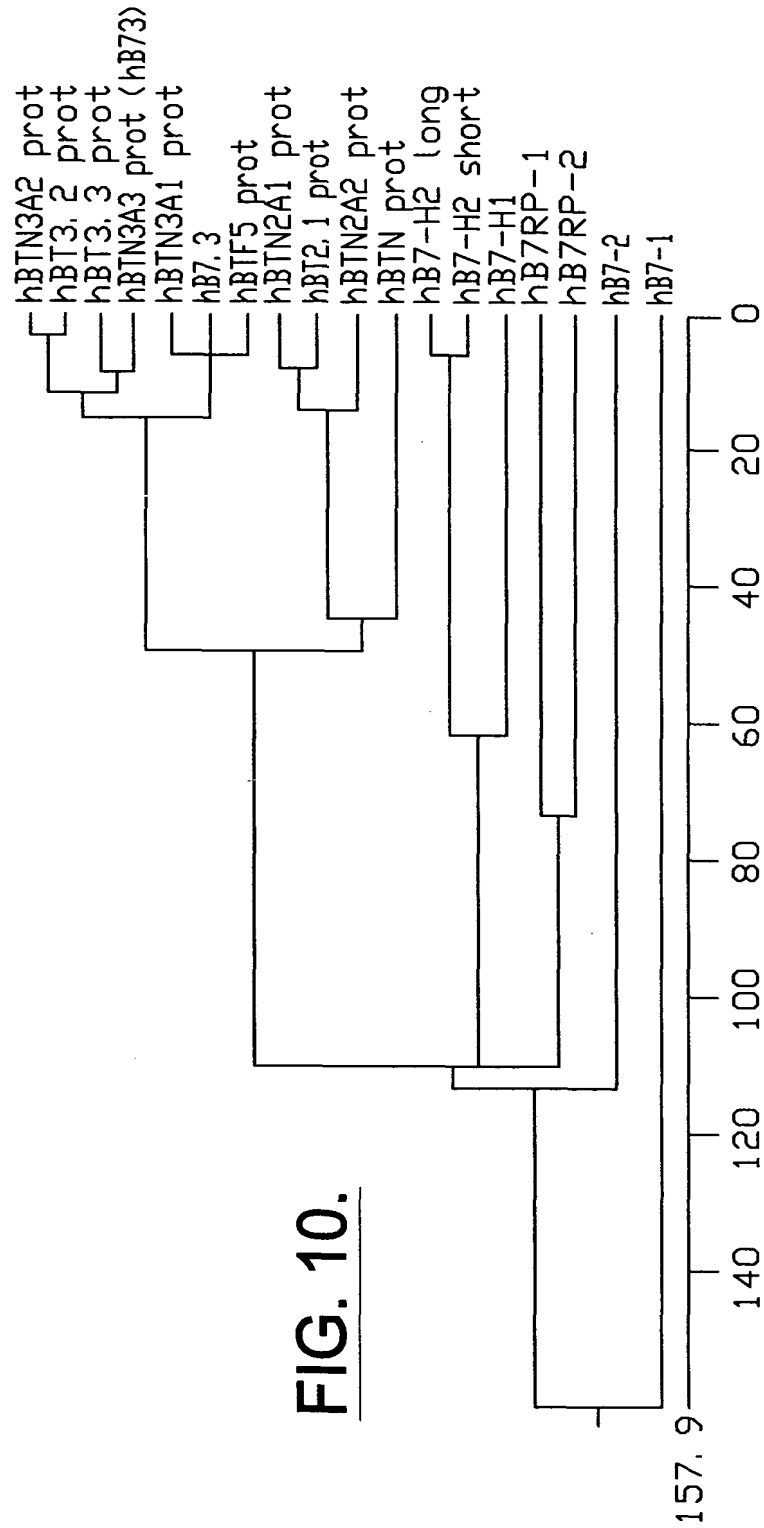


FIG. 9.



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## \*

\*

**FIG. 11A.**

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hB7-1	TLISVNGIFV	CC	TY	FAPRCRERRRNERL	---	RR	SVR	---	286
hB7-2	AVLP	---	TVI	CVMVF	---	WKWKKKRPRNSYK	GTNTMEREESEQTKKR	---	311
hB7RP-1	TGEKNATWS	I	LAV	-L	---	VVAVAIGMVC	DRCL	---	306
hB7RP-2	FPPE	---	ALW	TVGS	---	LI	VALAFVGM	---	305
hB7-H1	ER	---	LV	GGAL	---	AL	---	---	278
hB7-H2 long	PR	---	HT	WL	---	AF	---	---	262
hB7-H2 short	PR	---	HT	WL	---	AF	---	---	172
hB7-1	---	---	PV	---	---	---	---	---	289
hB7-2	K	---	SSC	---	---	---	---	---	323
hB7RP-1	---	---	LLS	---	---	---	---	---	309
hB7RP-2	DSKED	---	GGQEIA	---	---	---	---	---	317
hB7-H1	SKKQS	---	THLEET	---	---	---	---	---	290
hB7-H2 long	---	---	---	---	---	---	---	---	274
hB7-H2 short	---	---	---	---	---	---	---	---	183

Decoration 'Decoration #1': Shade (with dots) residues that match the Consensus exactly.

FIG. 11B.

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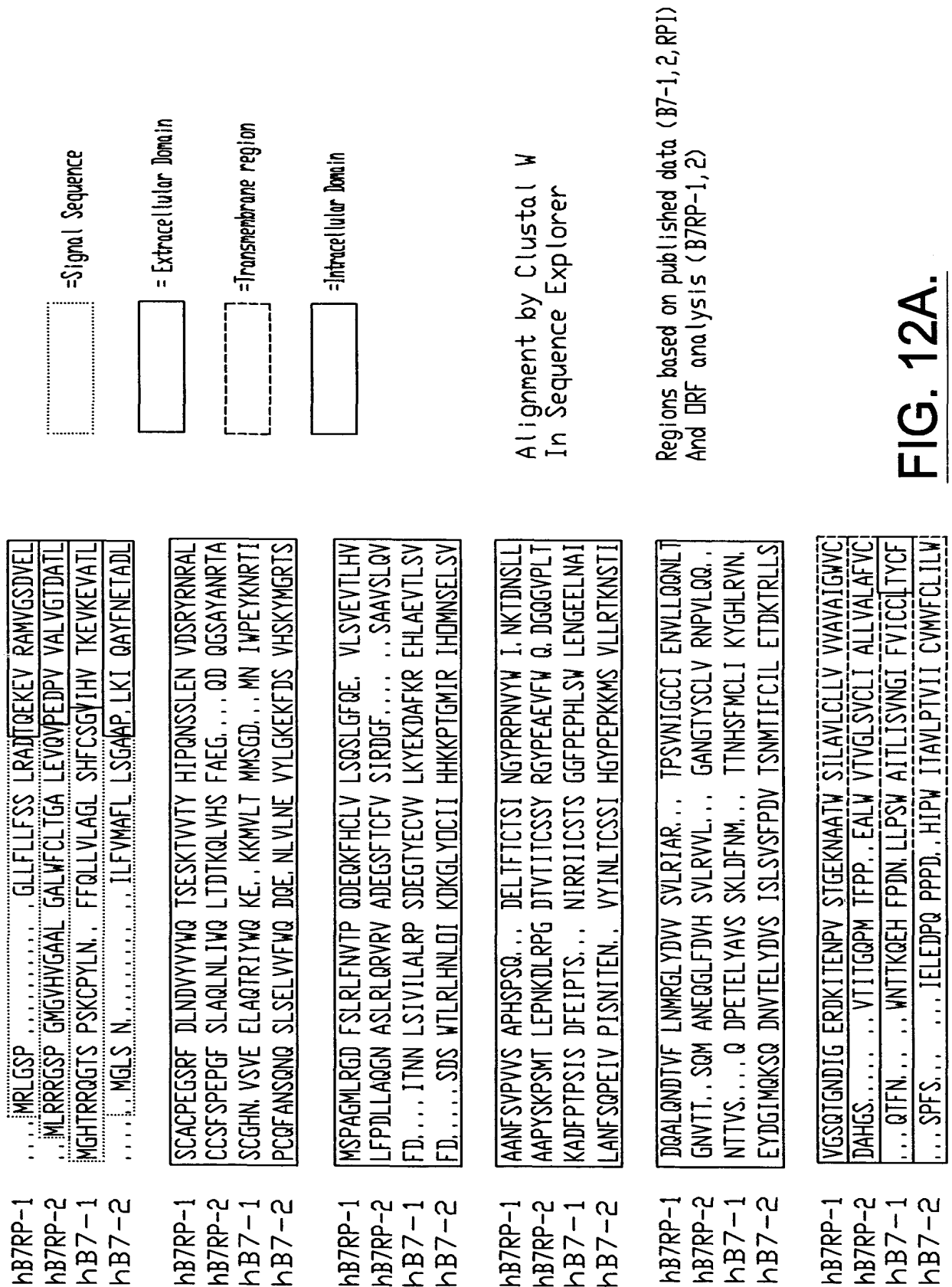


FIG. 12A.

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hB7RP-1	RDRCLQHS, Y AGAWAVSPET ELTGHV.....
hB7RP-2	WRKIKQSCEE ENAGAEEDQDG EGECSKTALQ PLKHSDSKED DGQEIA....
hB7-1	APRCRERRRN ERLRRESVRP V.....
hB7-2	KWKKKRPRN SYKCGTNTME REESEQTKKR EKIHIPERSD EAQRVFKSSK
hB7RP-1	.....
hB7RP-2	.....
hB7-1	.....
hB7-2	TSSCDKSDIC F

FIG. 12B.

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hB7-H1	VCHTRRRQETSSKCPYL---	NFQLLVAGLSHFCSGVIH	VTKETKEVAT	47
hB7-H2	MCLSN---	I---	VMAFSS	31
hB7RP-1	M---	RLGSPG	SSRADTQEKERAMVGS	34
hB7RP-2	N---	LRRCSPG	MGVHVGAAGLWCLTCALE	47
hB7-H1	LSGCHNV	SVVEE	LARTRIVWQ	90
hB7-H2	LPQQAAN	SNQCSL	SELVFWQ	79
hB7RP-1	LSQACPEGR	FDLNDVYVWQ	TSESKTVM	83
hB7RP-2	LCSESEPEGE	SLAQENLIWQLT	DTKQVHSFAE	92
hB7-H1	ITFB---	ITNLS	IVILALRRS	136
hB7-H2	TSST---	SDSWTL	RHNQIKDKGLYQC	124
hB7RP-1	ALMS	PAGMLR	EDFSRPFNVITPQDEQKH	132
hB7RP-2	WALF	PDLAQCNAS	LRQRVARADEST	136
hB7-H1	SVKADTP	TPSS	---	178
hB7-H2	SVLANF	SQPELV	---	172
hB7RP-1	HVAANF	SVPVVS	SAPHS	177
hB7RP-2	QVAA	PYSKPS	MTLEPNKDLRPG	184
hB7-H1	GEELNAT	NTTV	SQDPETE	225
hB7-H2	TIEYDGL	MQK	---	221
hB7RP-1	SLLDQAL	QNDTVFL	NMRGLYDVVS	224
hB7RP-2	PLTG	NVTTSQMA	---	229
hB7-H1	---	NQTE	NWNITKQEHF	274
hB7-H2	LSSP	ESIELED	PQPP	266
hB7RP-1	---	NLE	VGSQT	267
hB7RP-2	---	D-AH	GSV	261

FIG. 13A.

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hB7-H1	RRNER	-----R	SVR	-----	286								
hB7-H2	KKRPRNSYK	GTNTMERE	SQTKKR	REKIHIP	RSDEAQRVF	SKTSSC	316						
hB7RP-1	VVA	V	AIGW	V	CRDRCL	CHSYAGAWAVSPETELT	SWNLL	306					
hB7RP-2	LL	VA	AF	V	WRKIK	SC	EENAGAE	DQDGE	GGKTA	QPL	HS	DSKED	310
hB7-H1	----	PV											289
hB7-H2		KSDTCF											323
hB7RP-1	----	LLS											309
hB7RP-2		GGQEIA											317

Decoration 'Decoration #1: Shade residues that match the Consensus exactly.

FIG. 13B.

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hB7RP-2 vs hB7-1

Gap of: hB7RP-2 aa from: 1 to: 316 to: hB7-1 aa from: 1 to: 288

Percent Similarity: 32.734 Percent Identity: 24.820

```
1  ..MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDATL 48
    ||.|.          |  |  |          |  |  |||
1  MGHTRRQGTSPSKCPYLNFFQLL..VLAGLSHFCSGVIHVTKEVKEVATL 48
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
49 CCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALFPD 98
    |  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
49 SCGHNVSV.E.LAQTRIYWQ.KEKKMVLTMMSGDMNIWPEYKNRTIFD.. 94
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
99 LLAQGNASRLRLQVRVRADEGSFTCFV.....SIRDFGSAAVSLQVAAPY 142
    |  |  :  :  .  |  .  |||  :  |  |  .  .  :  .  |  |  |  |  |
95 ..ITNNLSIVILALRPSDEGTYESVVLKYEKDAFKREHLAEVTL SVKADF 142
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
143 SKPSMTLEPNKDLRPGDVTVTITCSSYRGYPEAEVFWQDGGQVPLTGNTT 192
    |||.  .  :  :  .  |  |||.  |  ||  .  |  :  |  |  ||
143 PTPSIS...DFEIPTSNIRRIICSTSGGFPEPHLSWLE.NGEELNAINTT 188
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
193 SQMANEQGLFDVHSLRVVLGANGTYSCLVRNPVLQQDAHGVSVTITGQPM 242
    |  |  :  |  |  |  .  :  |  .  :  |||  :  |  .  .  .  |  |
189 VSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHLRVNQTFNWNTTKQE. 237
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
243 TFPPEAL..WVTVGLSVCLIALLVAFVCWRKIKQSCEEENAGAEDQDG 290
    ||  |  |  |  :  ||  |  :  |  :  :  :  :  |  |
238 HFPDNLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRP 287
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
291 EGEKSKTALQPLKHSDSKEDDGQEI A 316
    .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
288 V..... 288
```

**FIG. 14.**



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## hB7RP-2 vs hB7-2

Gap of: hB7RP-2 aa from: 1 to: 316 to: hB7-2 aa from: 1 to: 323  
Percent Similarity: 31.186 Percent Identity: 21.695

1	MLRRRGSPGMGVHVGAA	LGALWFCLTGA	LEVQVPEDPVVALV	GT	DATLCC	50
		:   :	:   :	:   :		
1	.....MGLSNILFVMA	FLLSGAAPL	KIQAYFNETADLPC			34
51	SFSPEPGFSLAQLNLI	WQLTDTKQLVHSFA	EQQDQGSAYANRTA	LPD	LL	100
	.	:   .     :	:   :	:   :	:   :	
35	QFANSQNSLSELVVF	WQDQENLV	NEVYL	GKEK	FSVHSK. . YMGRTSF	82
101	AQGNASRLRQVRVA	DEGSFTCFVSIRD	.....FGSAAVSLQ	VAAPYSK		144
	. .	. . :   .   :	:   :	:   :	:   .	
83	DSDSWTLRLHNLQIK	DKGLYQCI	IHHKKPTGMIRI	HQMNSELSVLAN	FSQ	132
145	PSMTLEPNKDLRPGD	TVTITCSSYRGYPE	AE. . VFWQDGQGV	PLTGNVT		191
	.	. : :	: :	.	.	
133	PEIV. . PISNITENV	YINLTCSSIHGYEP	KKMSVLLRTKNST	IEYDGIM		180
192	TSQMANEQGLFDVHS	VLRVV. . LGANGTY	SCLVRNPVLQQDA	HGSVTIT		238
		:	. .	: .		
181	QKSQDNVTELYDVS	ISLSVSFPDVT	SNMTIFCILETDK	TRLLSSPFSIEL		230
239	GQPMTFPPEALWTV	GLSVCLIALLV	ALAFVCWRKIKQ	SCEEENAGAED		287
			:	:   . :	:     .	
231	EDPQPPPDHIPWIT	AVLPTVIICVMV	FCLILWKWKKKKR	PRNSYKCGTNT		280
288	QDGE	GE	GS	KTALQPLKHSDS	KE	DDGQEIA..... 316
	:	.   .		:   :	:	
281	MERE. ESEQTKKREK	IHIPERSDEAQRV	FKSSKTSSCDKSD	TCF		323

**FIG. 15.**

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hB7RP-1 vs hB7-2

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7-2 aa from: 1 to: 323

Percent Similarity: 31.250 Percent Identity: 21.181

```

      .       .       .       .
1  MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDVELSCACPEGSRFDLNDV  50
      :|  :||: . | .       .:|  :|  |  :|
1  ..MGLSNILFVM. AFLLSGAAPLKIQAYFNETADLPCQFANSQNQSLSEL  47

      .       .       .       .
51  YVYWQTSESKTVVTYHIPQNSSLENVDSRYRNRALMSPAGMLRGDFSLRL 100
      |:|  |. .       :. .       .:| |:| |  .:|
48  VVFWQDQENLVLNEVYL GK. EKFD SVHSKYMGR TSFD. .... SDSWTLRL  91

      .       .       .       .
101 FNVTPQDEQKFHCLV. LSQSLGFQEVLSVEVTLHVAANF SVP. VVSAPH S 148
      |. .| . :|: . | : . | | | | | :| .
92  HNLQIKDKGLYQCI IHHKKPTGMIRI HQMNSELSVL ANFSQPEIVPISNI 141

      .       .       .       .
149 PSQDEL TFTCTSINGYPRP. NVYWINKTDNSLLDQALQNDTVFLNMRGLY 197
      : ||. ||. || | . : :| || : : |. ||
142 TENVYINLTCSSIHGYPEPKMSVLLRTKNSTIEYDGIMQKSQDNVTELY 191

      .       .       .       .
198 DVVSVLRIARTPSVNIGCC IENVLLQQNLTVGSQTGNDIGERDKITENPV 247
      || | : | | | :| . | . | . :
192 DVSISLSVS. FPDVTSNMTIFCILETDKTRLLSSPF SIELED PQPPPDHI 240

      .       .       .       .
248 STGEKNAATWSILAVLCLLVVVAIGA WVC RDRLQHSYAGAWAVSPETE 297
      | . :|: | : | : | | . |
241 PWITAVLPT. ... VIICVMVFCLILWKWKKKRPRNSYKCGTNTMEREES 286

      .
298 LTGHV..... 302

      .
287 EQTKKREKIHIPERSDEAQRVFKSSKTSSCDKSDTCF 323
```

FIG. 16.

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hB7RP-1 vs hB7-1

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7-1 aa from: 1 to: 288

Percent Similarity: 30.292 Percent Identity: 24.088

```

      . . . . .
1  . . . . . MRLGSPGLLFLLFSSLRADTQEKEVRAMVGSDELSC 37
      . . . . . | . | . . . | | |
1  MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC 50
      . . . . .
38 ACPEGSRFDLNDVYVYWQTSESKTVVTYHIPQNSSLENVDSTRYRNRALMS 87
      | : | : || | | . | | : | : | :
51 G. HNVSVEELAQTRIYWQ. KEKKMVL. . . . MMSGDMNIWPEYKNRTIFD 94
      . . . . .
88 PAGMLRGDFSLRLFNVTPQDEQKFHCLVLS. QSLGFQEVLSVEVTLHVAA 136
      : . | : : . | || : | . | : | . | || | |
95 . . . . ITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKA 140
      . . . . .
137 NFSVPVVSAPHSPSQDELFTCTTSINGYPRPNVYWINKTDNSLLDQALQN 186
      . | | : | | . . | . | : | . | : | :
141 DFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWL. . ENGEELNAINT 187
      . . . . .
187 DTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGNDI 236
      | | | | | | . . | | . | . | | |
188 TVSQDPETELYAVSSKLDFNMTTNHSFMCLIKYGHRLVNQTFNWNTTKQE 237
      . . . . .
237 GERDKITENPVSTGEKNAATWSILAVLCLLVVVAIGAIGWVCRDRCLQHSY 286
      | : . | | . | : | | | | . | .
238 HFPDNLLPSWAIT. . LISVNGIFVICCLTYCFAPRCRERRRNERLRRES 284
      . . . . .
287 AGAWAVSPETELTGHV 302
      . . . . .
285 VRPV. . . . . 288
```

FIG. 17.

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# hB7RP-1 vs hB7RP-2

Gap of: hB7RP-1 aa from: 1 to: 302 to: hB7RP-2 aa from: 1 to: 316

Percent Similarity: 35.842 Percent Identity: 30.824

```

1 ..... MRLGSPGLLFLFSSLRADTQEKEVRAMVGSDVELSC 37
      .      | | | . |      | | | | | | |
1 MLRRRGSPGMGVHVGAAALGALWFCLTGALEVQVPEDPVVALVGTDLCC 50
      .      | | . . | | . . | .      . . | | | |
38 ACPEGSRFDLNDVYVYWQTSESKTVVTYHIPQNSSLENVDSRYRNRALMS 87
      .      | | . . | | . . | .      . . | | | |
51 SFSPEPGFSLAQLNLIWQLTDKQLV. . . HSFAEGDQDQGSAYANRTALF 96
      | : . | . | | | | | | | | | | . | | | | |
88 PAGMLRGDFSLRLFNVTPQDEQKFHCLVLSQSLGFQEVLSVEVTLHVAAN 137
      | : . | . | | | | | | | | | | . | | | | |
97 PDLLAQGNASRLRQVRVADEGSFTCFVSIRDFG. . . . SAAVSLQVAAP 141
      .      .      .      .      .      .      .      .
138 FSVPPVVSAPHSPS. . QDELTFTCTSINGYPRPNVYWINKTDNSLLDQAL 184
      : | | . . .      | . | | | | | | | | | | . |
142 YSKPSMTLEPNKDLRPGDVTITCSSYRGYPEAEVFWQDGGGVPLTGNVT 191
      .      .      .      .      .      .      .      .
185 QNDTVFLNMRGLYDVVSVLRIARTPSVNIGCCIENVLLQQNLTVGSQTGN 234
      .      | . | | | | | | | | | | . | : | . | | | . | | |
192 TSQ. . MANEQGLFDVHSLRVVLGANGTYSCLVARNPVLQQD. AHGSVT. . 236
      .      .      .      .      .      .      .      .
235 DIGERDKITENPVSTGEKNAATWSILAVLCLLVVVAVAIGWVCRDRCLQH 284
      | | | | . . .      | | . . .      | : . | | : . | |
237 ..... ITGQPMTFPPE. . ALWVTVGLSVCLIALLLVALAFVCWRKIKQS 277
      .      .      .      .      .      .      .      .
285 . SYAGAWAVSPETELTGHV. . . . . . . . . . . . . . . 302
      | | : | | |
278 CEEENAGAEDQDGEGEKSKTALQPLKHSDSKEDDGQEIA 316

```

**FIG. 18.**

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# hB7-1 vs hB7-2

Gap of: hB7-1 aa from: 1 to: 288 to: hB7-2 aa from: 1 to: 323

Percent Similarity: 33.579 Percent Identity: 22.878

```

      .           .           .           .
1  MGHTRRQGTSPSKCPYLNFFQLLVLAGLSHFCSGVIHVTKEVKEVATLSC 50
      :           :| .           : :           ||||
1  ..... MGLSNILFVMAFLLSGAAPLKIQAYFNETADLPC 34
      .           .           .           .
51  GH. NVSVEELAQTRIYWQKEKKMVLTM. ... SGDMNIWPEYKNRTIFDI 95
      | : | : :|| : : || .           : : | |||
35  QFANSQNQSLSELVFWQDQENLVNEVYLGKEKFDVHSKYMGRTSFD. 83
      .           .           .           .
96  TNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTL SVKADFPTP 145
      ... : : | . | . | :|| : .           | | ||| | . |
84  SDSWTLRLHNLQIKDKGLYQCIIHKKPTGMIRIHQMNSELSVLNFSQP 133
      .           .           .           .
146  SISDFEIPTSNIR. RIICSTSGGFPEPHLSWLENGEELNAIN. ... TTVS 190
      | | : || : ||| .           . . |
134  EIVPISNITENVYINLTCSSIHGYPEPKKMSVLLRTKNSTIEYDGIMQKS 183
      .           .           .           .
191  QDPETELYAVSSKLDF. ... NMTTNHSFMCLIKYGHLR. VNQTFNWNTTKQ 236
      || |||| || | . . | . | : : | . . |
184  QDNVTELYDVSISLSVSFPDVTSNMTIFCILETDKTRLLSSPFSIELEDP 233
      .           .           .           .
237  EHFPDNLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVR 286
      : || : : | : : | : : : | | .
234  QPPPDHIPWITAVLPTVIICVMVFCLILWKWKKKKRPRNSYKCGTNTMER 283
      .           .           .           .
287  PV..... 288
      .           .           .           .
284  EESEQTKKREKIHIPERSDEAQRVFKSSKTSSCDKSDTCF 323

```

FIG. 19.

mB7RP-2 Nucleotide sequence

ATGCTTCGAGGATGGGGTGGCCCCAGTGTGGGTGTGTGTGTGCGCACAGCGCTGGGGGT  
GCTGTGCCTCTGCCTCACAGGAGCTGTGGAAGTCCAGGTCTCTGAAGACCCCGTGGTGG  
CCCTGGTGGACACGGATGCCACCCTACGCTGCTCCTTTTCCCCAGAGCCTGGCTTCAGT  
CTGGCACAGCTCAACCTCATCTGGCAGCTGACAGACACCAAACAGCTGGTGCACAGCTT  
CACGGAGGGCCGGGACCAAGGCAGTGCCTACTCCAACCGCACAGCGCTCTTCCCTGACC  
TGTTGGTGCAAGGCAATGCGTCCTTGAGGCTGCAGCGCGTCCGAGTAACCGACGAGGGC  
AGCTACACCTGCTTTGTGAGCATTACAGGACTTTGACAGCGCTGCTGTTAGCCTGCAGGT  
GGCCGCCCCCTACTCGAAGCCCAGCATGACCCTGGAGCCCAACAAGGACCTACGTCCAG  
GGAACATGGTGACCATCACGTGCTCTAGCTACCAGGGCTATCCGGAGGCCGAGGTGTTT  
TGGAAGGATGGACAGGGAGTGCCCTTGACTGGCAATGTGACATCCCAGATGGCCAACGA  
GCGGGGCTTGTTTCGATGTTTCACAGCGTCTGAGGGTGGTGCTGGGTGCTAACGGCACCT  
ACAGCTGCCTGGTACGCAACCCGGTGTTCAGCAAGATGCTCACGGCTCAGTCACCATC  
ACAGGGCAGCCCCTGACATTCCCCCCTGAGGCTCTGTGGGTAACCGTGGGGCTCTCTGT  
CTGTCTTGTGGTACTACTGGTGGCCCTGGCTTTCGTGTGCTGGAGAAAGATCAAGCAGA  
GCTGCGAGGAGGAGAATGCAGGTGCCAAGGACCAGGATGGAGATGGAGAAGGATCCAAG  
ACAGCTCTACGGCTCTGAAACCTCTGAAAACAAAGAAGATGACGGACAAGAAATTGC  
TTGA

**FIG. 20.**

mB7RP-2 Protein sequence

MLRGWGGPSVGVCVRTALGVLCCLTGAVEVQVSEDPVVALVDTDATLRCSFSPEPGFS  
LAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSNRALFPDLLVQGNASRLQRVRVTDEG  
SYTCFVSIQDFDSAAYSLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVF  
WKDGQGVPLTGNVTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNPVLQQDAHGSVTI  
TGQPLTFPPEALWTVGLSVCLVLLVALAFVCWRKIKQSCEEENAGAKDQDGDGEGSK  
TALRPLKPSENKEDDGQEIA.

**FIG. 21.**

Gap of: mB7RP-2 aa from: 1 to: 315 to: hB7RP-2 aa from: 1 to: 316  
Percent Similarity: 89.841 Percent Identity: 88.254

[illegible]

FIG. 22.

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mB7RP-1 vs mB7RP-2

Gap of: mB7RP-1 aa from: 1 to: 322 to: mB7RP-2 aa from: 1 to: 315

Percent Similarity: 32.192 Percent Identity: 27.740

```

      .           .           .           .
1  MQLKCPCFVSLGTRQPVWKKLHVSSGFFSGLGLFLLLLSSLCAAS. AETE  49
      |   |   . ||.  ||.   .|
1  .....MLRGWGGPSVGVCVRTALGVLCCLTGAVEVQVSEDP  37
      .           .           .           .
50 VGAMVGSNNVLSCIDPHRRHFNLSGLYVYWQIENPEVSVTYYPYKSPGI  99
   | ||. .  | |   . |. | . ||. .  | : : |
38 VVALVDTDATLRCSFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQG.  86
      .           .           .           .
100 NVDSSYKNRGHLSLDSMKQGNFSLYLKNVTPQDTQEFTCRVFMNTATELV 149
    |. | || | | : ||| || |. | | : || |
87 ...SAYSNRTALFPDLLVQGNASRLQRVRVTDEGSYTCFV.....SIQ 127
      .           .           .           .
150 KILEEVRLRVAANFSTPVIISTDSSN..PGQERTYTCMSKNGYPEPNLY 197
    | |. ||| : | | . .  || | || | ||| .
128 DFDSAASLQVAAPYSKPSMTLEPNKDLRPGNMVTITCSSYQGYPEAEVF 177
      .           .           .           .
198 WINTTDSLIDTALQNNTVYLNKLGlyDVISTLRLPWTSRGDVLCCVENV 247
    | | | :   .  |. ||: || | ||. .  | || |
178 W...KDGQGVPLTGNVTSQMANERGLFDVHSVLRVVLGANGTYSCLVRNP 224
      .           .           .           .
248 ALHQNITSISQAESFTGNNTKNPQETHNNELKVLVPVLAVLAAAFVSFI 297
    | |. . . || | | . . |. . . | || |
225 VLQQDAHG...SVTITGQPLTFPEALWVTVGLSVCLVLLVALAFVCWR 271
      .           .           .           .
298 IYRRTRPHRSYTGPKTVQLELTDHA..... 322
    :. . . | | :
272 KIKQSCEEEN. AGAKDQDGDGEGSKTALRPLKPSENKEDDGQEIA 315

```

**FIG. 23.**



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mB7-H2 orf

ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACCTTCATCCTGTAGCAGCTTTATTCACCGTGACA  
GCCCCCTAAAGAAGTGTACACCGTAGACGTCGGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAA  
TGCACTGAAC TGGAAGGGATAAGAGCCAGTTTGCAGAAGGTAGAAAATGATACGTCTCTGCAAAGTGAAAGA  
GCCACCCTGCTGGAGGAGCAGCTGCCCCTGCGAAAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGAT  
TCCGGGCAGTACCGTTGCCTGGTCATCTGCGGGGCCGCTGGGACTACAAGTACCTGACGGTGAAAGTCAAA  
GCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTTCCAGGTACAGGGGAGGTGCAGCTTACCTGCCAG  
GCTAGAGGTTATCCCCTAGCAGAAGTGTCTGGCAAAATGTCAGTGTTCTGCCAACACCAGCCACATCAGG  
ACCCCCGAAGGCCTCTACCAGGTCACCAAGTGTCTGCGCCTCAAGCCTCAGCCTAGCAGAACTTCAGCTGC  
ATGTTCTGGAATGCTCACATGAAGGAGCTGACTTCAGCCATCATTGACCCTCTGAGTCGGATGGAACCCAAA  
GTCCCCAGAACGTGGCCACTTCATGTTTTTCATCCCGGCTGCACCATCGCTTTGATCTTCCTGGCCATAGTG  
ATAATCCAGAGAAAGAGGATCTAG

FIG. 24.

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mB7-H2 Protein Sequence

Met	Ile	Phe	Leu	Leu	Leu	Met	Leu	Ser	Leu	Glu	Leu	Gln	Leu	His	Gln
1				5					10					15	
Ile	Ala	Ala	Leu	Phe	Thr	Val	Thr	Val	Pro	Lys	Glu	Leu	Tyr	Ile	Ile
			20					25					30		
Glu	His	Gly	Ser	Asn	Val	Thr	Leu	Glu	Cys	Asn	Phe	Asp	Thr	Gly	Ser
		35					40					45			
His	Val	Asn	Leu	Gly	Ala	Ile	Thr	Ala	Ser	Leu	Gln	Lys	Val	Glu	Asn
	50					55					60				
Asp	Thr	Ser	Pro	His	Arg	Glu	Arg	Ala	Thr	Leu	Leu	Glu	Glu	Gln	Leu
65					70					75					80
Pro	Leu	Gly	Lys	Ala	Ser	Phe	His	Ile	Pro	Gln	Val	Gln	Val	Arg	Asp
				85					90					95	
Glu	Gly	Gln	Tyr	Gln	Cys	Ile	Ile	Ile	Tyr	Gly	Val	Ala	Trp	Asp	Tyr
			100					105					110		
Lys	Tyr	Leu	Thr	Leu	Lys	Val	Lys	Ala	Ser	Tyr	Arg	Lys	Ile	Asn	Thr
		115					120					125			
His	Ile	Leu	Lys	Val	Pro	Glu	Thr	Asp	Glu	Val	Glu	Leu	Thr	Cys	Gln
	130					135					140				
Ala	Thr	Gly	Tyr	Pro	Leu	Ala	Glu	Val	Ser	Trp	Pro	Asn	Val	Ser	Val
145					150					155					160
Pro	Ala	Asn	Thr	Ser	His	Ser	Arg	Thr	Pro	Glu	Gly	Leu	Tyr	Gln	Val
				165					170					175	
Thr	Ser	Val	Leu	Arg	Leu	Lys	Pro	Pro	Pro	Gly	Arg	Asn	Phe	Ser	Cys
			180					185					190		
Val	Phe	Trp	Asn	Thr	His	Val	Arg	Glu	Leu	Thr	Leu	Ala	Ser	Ile	Asp
	195						200					205			
Leu	Gln	Ser	Gln	Met	Glu	Pro	Arg	Thr	His	Pro	Thr	Trp	Leu	Leu	His
	210					215					220				
Ile	Phe	Ile	Pro	Ser	Cys	Ile	Ile	Ala	Phe	Ile	Phe	Ile	Ala	Thr	Val
225					230					235					240
Ile	Ala	Leu	Arg	Lys	Gln	Leu	Cys	Gln	Lys	Leu	Tyr	Ser	Ser	Lys	Asp
				245					250					255	
Thr	Thr	Lys	Arg	Pro	Val	Thr	Thr	Thr	Lys	Arg	Glu	Val	Asn	Ser	Ala
			260					265					270		
Ile															

**FIG. 25.**

mB7-H2 orf vs hB7-H2 long orf

Gap of: hB7-H2 long from: 1 to: 822 to: mB7-H2 from: 1 to: 744

Percent Similarity: 78.331 Percent Identity: 78.331

```

      .       .       .       .
1  ATGATCTTCCTCCTGCTAATGTTGAGCCTGGAATTGCAGCTTCACCAGAT  50
   ||| |  ||||  ||||  ||  |||  ||||  ||  ||  |||||  |  |
1  ATGCTGCTCCTGCTGCCGATACTGAACCTGAGCTTACAACCTTCATCCTGT  50

      .       .       .       .
51 AGCAGCTTTATTACAGTGACAGTCCCTAAGGAACTGTACATAATAGAGC 100
   |||||  |||||  |||||  |||||  |||  |||||  |||||
51 AGCAGCTTTATTACCGTGACAGCCCCTAAAGAAGTGTACACCGTAGACG 100

      .       .       .       .
101 ATGGCAGCAATGTGACCCTGGAATGCAACTTTGA. CACTGGAAGTCATGT 149
     |||||  |||||  |||||  |||  |  |||||  |  |  |  |  |
101 TCGGCAGCAGTGTGAGCCTGGAGTGCGATTTTGACCGCAGAGAATGCACT 150

      .       .       .       .
150 GAACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACAT 199
     |||  ||  |  ||  ||||  |||||  |||||  |||||  |||||  |||
151 GAA. CTGGAAGGGATAAGAGCCAGTTTGCAAGGTAGAAAATGATACGT 199

      .       .       .       .
200 CCCCACACCGTGAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTAGGG 249
   |  |  ||  |||||  |||||  |||||  |||||  |||||  |||||  ||
200 CTCTGCAAAGTGAAAGAGCCACCCTGCTGGAGGAGCAGCTGCCCTGGGA 249

      .       .       .       .
250 AAGGCCTCGTTCCACATACCTCAAGTCCAAGTGAGGGACGAAGGACAGTA 299
   |||||  |  |||||  |||||  |||  |||||  |||||  ||  ||  |||||
250 AAGGCTTTGTTCCACATCCCTAGTGTCCAAGTGAGAGATTCCGGGCAGTA 299

      .       .       .       .
300 CCAATGCATAATCATCTATGGGGTCGCCTGGGACTACAAGTACCTGACTC 349
   ||  |||  |  |||||  ||||  |||||  |||||  |||||  |||||  ||
300 CCGTTGCCTGGTCATCTGCGGGGCCGCCTGGGACTACAAGTACCTGACGG 349

      .       .       .       .
350 TGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATCCTAAAGGTT 399
   |||||  |||||  |||||  ||||  ||  |||  |||||  |||||  |||||
350 TGAAAGTCAAAGCTTCTTACATGAGGATAGACACTAGGATCCTGGAGGTT 399

```

**FIG. 26A.**

400 CCAGAAACAGATGAGGTAGAGCTACCTGCCAGGCTACAGGTTATCCTCT 449  
|||| ||| |||| ||| ||||||||| ||||||| ||  
400 CCAGGTACAGGGGAGGTGCAGCTTACCTGCCAGGCTAGAGGTTATCCCCT 449  
450 GGCAGAAGTATCCTGGCCAAACGTCAGCGTTCCTGCCAACACCAGCCACT 499  
||||||| ||||||| || ||||| ||||||||| ||||||| ||  
450 AGCAGAAGTGTCTGGCAAATGTCAGTGTTCCTGCCAACACCAGCCACA 499  
500 CCAGGACCCCTGAAGGCCTCTACCAGGTCACCAGTGTTCGCGCCTAAAG 549  
||||||| ||||||||| ||||||||| ||||||||| ||||| |||  
500 TCAGGACCCCGAAGGCCTCTACCAGGTCACCAGTGTTCGCGCCTCAAG 549  
550 CCACCCCTGGCAGAACTTCAGCTGTGTTCCTGGAATACTCACGTGAG 599  
|| | ||| ||||||||| ||||||||| ||||| |||  
550 CCTCAGCCTAGCAGAACTTCAGCTGCATGTTCTGGAATGCTCACATGAA 599  
600 GGAACCTACTTTGGCCAGCATTGACCTTCAAAGTCAGATGGAACCCAGGA 649  
||| || |||| |||| ||||||| || |||| |||||||||  
600 GGAGCTGACTTCAGCCATCATTGACCTCTGAGTCGGATGGAACCCAAAG 649  
650 CCCATCCAACCTGGCTGCTTCACATTTTCATCCCCTCCTGCATCATTGCT 699  
|| ||| |||| |||| ||||||| ||||| ||| |||  
650 TCCCAGAACGTGGCCACTTCATGTTTTCATCCCGGCCTGCACCATCGCT 699  
700 TTCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAA 749  
|| || ||| || |||| |||||| || |||| |||  
700 TTGATCTTCCTGGCCATAGTGATAATCCAGAGAAAGAGGATCTAG..... 744

FIG. 26B.

mB7-H2 vs hB7-H2 long

Gap of: mB7-H2 aa from: 1 to: 247 to: hB7-H2 long aa from: 1 to: 273

Percent Similarity: 74.899 Percent Identity: 69.636

```
1  MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDRRECT  50
   | | . | . | | | | : | | | | | | | | . | : | | . | | | . | |
1  MIFLLMLSLQLHQIAALFTVTPKELYIEHGSNVTLECNFDTGSHV  50

51  ELEGIRASLQKVENDTSLQSERATLLEEQLPLGKALFHIPSVQVRDSGQY 100
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
51  NLGAITASLQKVENDTSPHRERATLLEEQLPLGKASFHIPQVQVRDEGQY 100

101 RCLVICGAADYKYLTVKVKASYMRIDTRILEVPGTGEVQLTCQARGYPL 150
   . | : : | | | | | | | | | | | | | | | | | | | | | | | |
101 QCIIYGVADYKYLTLKVKASYRKINTHILKVPETDEVELTCQATGYPL 150

151 AEVSWQNVSVPAANTSHIRTPEGLYQVTSVLRCLKPQPSRNFSCMFVNAHMK 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 AEVSWPNVSVPAANTSHSRTPPEGLYQVTSVLRCLKPPPGRNFSCVFWNTHVR 200

201 ELTSAIIDPLSRMEPKVPRTWPLHVFIPACTIALIFLAIVIIQRKRI... 247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
201 ELTLASIDLQSQMEPRTHPTWLLHIFIPSCIIAFIFATVIALRKQLCQK 250
```

⋮

FIG. 27.

mB7-H2 vs mB7-H1

Gap of: mB7-H2 aa from: 1 to: 247 to: mB7-H1 aa from: 1 to: 290  
Percent Similarity: 44.262 Percent Identity: 34.016

```

      .       .       .       .
1  . MRIFAGIIFTACCHLLRA. FTITAPKDLVVEYGSNVTMECRFPVEREL  48
      : : : : | . | ||:||||:| | : ||.:|| |
1  MLLLLPILNLSLQLHPVAALFTVTAPKEVYTVDVGSSVSLECDFFRRECT  50

      .       .       .       .
49 DLLALVYWEKEDEQVIQFVAGEEDLKQHSNFRGRASLPKDQLLKGNAA  98
      :| : : : : :| | : |. : : ||. | :|| | |
51 ELEGI.....RASLQKVENDTSLQSE.....RATLLEEQLPLGKAL  86
      .       .       .       .
99 LQITDVKLQDAGVYCCIISYGA. DYKRITLKVNPYRKINQRISVDPAT 147
      | |...|. | | | : | | | | | | | | : |. | | |
87 FHIPSVQVRDSGQYRCLVICGAAWDYKYLTVKVKASYMRIDTRILEVPGT 136

      .       .       .       .
148 SEHELICQAEGYPEAEVIWTNSDHQPVSGKRSVTTSRTEGMLLNVTSSLR 197
      | :| ||| ||| ||| | | | | . . || | ||| ||
137 GEVQLTCQARGYPLAEVSWQN....VSPANTSHIRTPEGLYQVTSVLR 181
      .       .       .       .
198 VNATANDVFYCTFWRSQPGQNHTAELIPELPATHPPQNRTHWVLLGSIL 247
      . . | | | | . : . | : : |. | : .
182 LKPQPSRNFSCMFVNAHMKELTSAIIDPLSRMEPKVPRTWPLHVFIPACT 231

      .       .       .       .
248 LFLIVSTVLLFLRKQVRMLDVEKCGVEDTSSKNRNDTQFEET 290
      : || . . | : | : | :
232 IALIFLAIVII. QRKRI.....247

```

**FIG. 28.**

mB7-H2 vs mB7RP-2

Gap of: mB7-H2 aa from: 1 to: 247 to: mB7RP-2 aa from: 1 to: 298

Percent Similarity: 32.245 Percent Identity: 24.490

```

      .       .       .       .
1  MLRGWGGPSVGVCVRTALGVLCLCLTGAVEVQVSEDPVVALVDTDATLRC  50
      | | . . . | | | |
1  ..... MLLLLPILNLSLQLHPVAALFTVTAPKEV  29
      .       .       .       .
51 . SFSPEPGFSLAQLNLIWQLTDTKQLVHSFTEGRDQGSAYSNRTALFPDL  99
      | | . . . | | . . | | | |
30 YTVDVGSSVSLECDFDRRECTELEGIRASLQKVENDTSLQSERATLLEEQ  79
      .       .       .       .
100 LVQGNASRLRQVRVTDEGSYTCFVSI. QDFDSAASLQVAAPYSKPSMT 148
      | | | | . | | | | | . . . . | | |
80 LPLGKALFHIPSVQVRDSGQYRCLVICGAADYKYLTVKVKASYMRIDTR 129
      .       .       .       .
149 LEPNKDLRPGNMVTITCSSYQGYPEAEVFWKDGQGVPLTGNVTSQMANER 198
      : . . | : | | . | | | | | | | . | | |
130 I... LEVPGTGEVQLTCQA. RGYPLAEVSW... QNVSVPAN. TSHIRTP 171
      .       .       .       .
199 GLFDVHSVLRVVLGANGTYSLVRNPVLQQDAHGSVTITGQPLTFPPEAL 248
      ||: | ||| . . : ||: | : : . . |
172 GLYQVTSVLRLKPQPSRNFSCMFNAHMKELTSAAIIDPLSRMEPKVPRTW 221
      .       .       .       .
249 WVTVGLSVCLVLLVALAFVCRKIKQSCÉEENAGAKDQDGDGEGSKTAL 298
      . | : | : | : . | |
222 PLHVFIPACTIALIFLAIVIIQRKRI..... 247

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⋮

FIG. 29.